Wildlife Health Bulletin 04- 01

To: Natural Resource/Conservation Managers
From: Leslie Dierauf, Director, USGS National Wildlife Health Center
Title: Avian Influenza in Wild Birds

A strain of avian influenza virus (H5N1) in Asia has recently killed or resulted in the depopulation of millions of domestic chickens. Human deaths due to H5N1virus have also been reported. The potential spread of this virus is of international concern.

While it is common for wild birds, particularly waterbirds, to carry strains of avian influenza virus, there is little evidence that the **new** virulent H5N1 virus strain is affecting wild bird populations, or that wild birds are able to spread this Highly Pathogenic Avian Influenza (HPAI) virus. Thus far in 2004, there is a report that out of 6000 wild birds tested in Hong Kong, one peregrine falcon was positive for the H5N1 strain. It is not known how the bird became infected and reports are not clear if the bird actually died from the disease.

Currently there is no evidence that humans have been infected with the H5N1 influenza virus through contact with wild birds. All reported human infections have been associated with contact with domestic poultry.

Direct Infection of Humans
Historically, it was considered very unusual for avian influenza to directly infect humans. However, recent reports [Hong Kong (H5N1), 1997; Hong Kong/China (H9N2), 1999; Netherlands (H7N7), 2003; Asia (H5N1), 2003-2004] indicate that at least some people who have had contact with domestic poultry have become directly infected with virulent avian influenza virus. To date, these viruses have not acquired the capacity to effectively spread directly from human to human.

Possible Impacts to Wild Birds
Historically, avian influenza viruses recovered from wild waterbirds have rarely caused disease. The only reported die-off was in common terns in South Africa in 1961 (Friend, 1999). Little is known about the potential impact the recent H5N1 avian influenza virus found in Asia may have on wild birds. There is a concern that a genetic shift in the virus may have occurred during replication in domestic poultry, making this avian influenza virus virulent to waterbirds.

In January 2004, ProMed (Archive No. 20040121.0243) reported that of the 6,000 wild birds tested during extensive surveillance and testing of wild birds (unspecified species) in Hong Kong only 1 dead peregrine falcon was positive for the for the H5N1 avian influenza virus. The falcon was found near two chicken farms and it is not known how it became infected. It is also not clear if the bird actually died from the disease. A 2002 report (http://www.oie.int/eng/info/hebdo/AIS_07.HTM#Sec0 and

www.oie.int/eng/info/hebdo/AIS_35.HTM#Sec0) suggests that a strain of H5N1 killed non-domestic birds in parks and a zoological collection in Hong Kong, including waterfowl, greater flamingos, gray herons and egrets. There is no definite evidence that the 2003/2004 virulent H5N1 virus is affecting wild bird populations, or that wild birds are able to disseminate this **new** Highly Pathogenic Avian Influenza (HPAI) virus.

Wild Bird Reservoir

Avian influenza viruses circulate freely in populations of free-flying waterbirds (primarily ducks and shorebirds) throughout the world. The different virus subtypes circulate independently of one another and move within, and sometimes among, the flyways of the North American and Eurasian continents. In addition, the number and antigenic characteristics of avian influenza subtypes vary annually. Subtypes of this virus are defined by their Hemagglutinin (H) and neuraminidase (N) proteins/ antigens. All 15 of the known avian influenza Hemagglutinin and 9 known neuraminidase virus proteins have been found in viruses isolated from wild ducks. Most of the H and all of the N antigens have been identified in viruses isolated from shorebirds.

Waterbirds appear to contain and maintain the genetic pool of avian influenza subtypes from which future influenza strains that affect poultry and humans could evolve. Within natural populations of wild birds, these viruses appear to be stable. However, the virus mutation rate increases when it is transferred and adapts to a new host species, which can result in increased virulence. Viruses responsible for disease outbreaks in domestic poultry and human infections have segments of genes that can be traced (phylogenetically) to strains of avian influenza virus historically found in wild waterbirds.

Virus Virulence

Virulence is the ability of an organism, in this case avian influenza virus, to cause disease. A virus can increase its virulence in a number of ways, such as increasing its ability to transmit to uninfected animals, increasing the amount of virus shed from infected animals and increasing the severity of disease in an animal, or by increasing the range of hosts it can infect. Two types of genetic mutation, genetic drift and genetic shift, can lead to increased virulence of avian influenza virus.

Virus Drift – High-density populations with high rates of virus replication

When an influenza virus is introduced to domestic fowl, multiple passages (generations) of virus occur through sequential infection of individual birds in that population, which provides an excellent opportunity for the virus to genetically mutate. This can happen quite rapidly when poultry are housed at high densities in confined quarters, allowing the virus to spread quickly. As the virus progresses through a poultry flock, small changes in the virus genetic material, known as “genetic drift”, may result in the appearance of a virus strain that is highly pathogenic to poultry. Some strains of HPAI have the ability to cause 90% mortality in domestic farmed fowl. Infected fowl can become virus pumps producing and shedding large quantities of infectious virus that contaminate the local environment, facilitating transmission of the virus within the population, which also increases the probability of virus spreading to sites/farms beyond the location of the

original outbreak. This geographic spread is rapid in situations of poor management practices or movement (smuggling) of infected birds.

Virus Shift – Different species acting as mixing vessels for virus genes
Increased virulence may occur when genes from two different influenza strains reassort during co-infection in a single host, expanding the range of animals the virus can infect. A classic example of a viral mixing vessel for this gene reassortment is swine (Figure 1). If a swine influenza virus and an avian influenza virus simultaneously infect a pig, the two different influenza viruses can swap genetic material as they both replicate in the pig host. This is an example of genetic shift. If the avian influenza virus acquires genes required for mammalian infection and transmission, the new avian influenza virus may gain the unique ability to spread easily between mammals, possibly including humans (Figure 2).

Evidence suggests that domestic quail can also become mixing vessels for avian influenza viruses because they have the potential to become infected by multiple avian influenza subtypes. One report proposes that the simultaneous infection of domestic quail with influenza subtypes from geese, ducks, and quail provided the opportunity for genetic shift in the quail virus resulting in increased virulence in new hosts, including poultry and humans (Webby and Webster, 2001). This is believed to have been the source for avian influenza viruses that infected humans in Hong Kong in 1997 and 1999.

There is concern that humans could assume a role similar to swine and domestic quail by becoming the "vessel" for mixing avian and human influenza genes. This would provide the opportunity for a genetic shift in the avian influenza virus to a virus that is highly virulent and transmissible to and among humans, possibly sparking the next influenza pandemic.

There are situations that provide an ideal opportunity for individuals to become simultaneously infected with multiple influenza virus strains. Human contact with live bird markets that house numerous bird species in close contact, co-located poultry (backyard flocks) and swine, and high density poultry operations are ideal for potential genetic shift, allowing the virus to jump species.

What is needed
New information is needed that addresses the potential for the current H5N1 virus to kill wild waterbirds, and determine whether wild waterbirds play a significant role in dissemination of this virus. Surveillance of wild birds, particularly during mortality events, needs to be conducted to monitor for the appearance of H5N1 subtypes, followed by laboratory tests to assess the virulence of this virus in wild birds, and to determine the potential role wild birds may play in disseminating this new virus.

The outbreak of avian influenza in Asia, along with the recent emergence of other high-profile zoonotic diseases such as West Nile virus and severe acute respiratory syndrome (SARS) has increased the importance of understanding the interactions among humans, domestic animals, and wildlife in the maintenance and transmission of disease and

illustrates the need for collaboration among wildlife, agricultural and human health agencies.

Figure 1. **Historical** influenza disease cycle

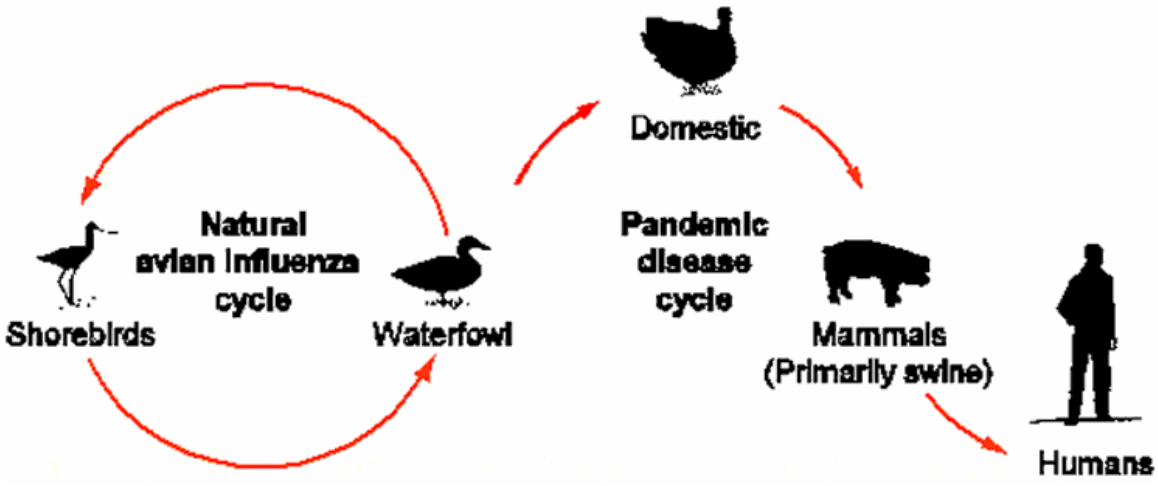
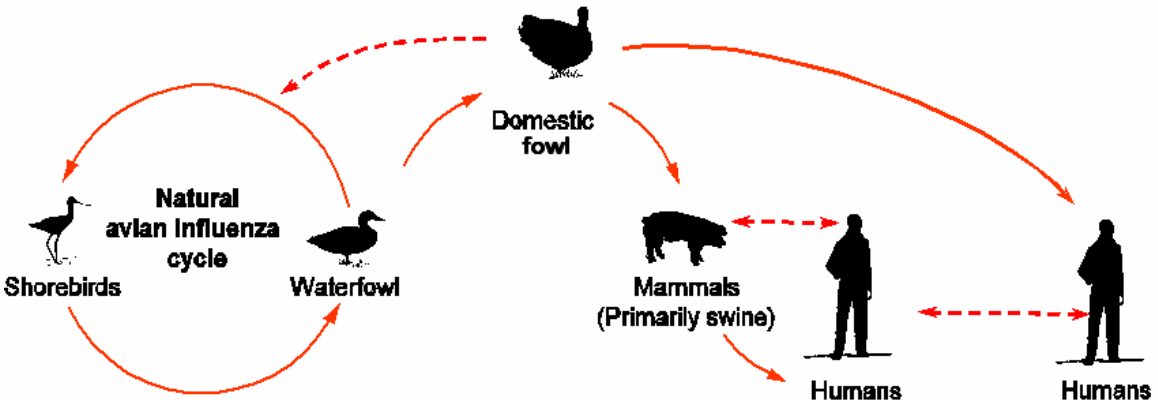


Figure 2. **Current and future concerns** about the transmission of avian influenza virus (H5 N1)



For additional information, contact Christopher Brand, 608-270-2440, or Paul Slota, 608-270-2420, at the National Wildlife Health Center.

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References

Friend, M. 1999. Field Manual of Wildlife Diseases. General Field Procedures and Diseases of Birds, U.S. Department of the Interior, U.S. Geological Survey Information and Technology Report 1999-001.

Webby, R.J.,Webster,R.G. 2001 Emergence of influenza A viruses. Philosophical Tansactions of the Royal Society of London B Biological Sciences 356, 1817-1828.

Swayne, D.E.,Halverson, D.A., 1999. Influenza in Diseases of Poultry 11th Edition, pp. 135-160. Edited by Y.M. Saif, Iowa State Press, Blackwell Publishing Company, USA.

Links to more information:

Avian Influenza (pdf file)
Chapter 22 of The Field Guide to Wildlife Diseases

Center for Disease Control - Avian Influenza (Bird Flu) Outbreak

USDA Avian Influenza Factsheet

OIE World Organization for Animal Health